

H2afy2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

H2afy2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *H2afy2* gene. The schematic diagram is as follows:



- The *H2afy2* gene has 1 transcript. According to the structure of *H2afy2* gene, exon3-exon5 of *H2afy2-201* (ENSMUST00000020283.4) transcript is recommended as the knockout region. The region contains 416bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *H2afy2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele do not exhibit any developmental or reproductive abnormalities.
- The *H2afy2* gene is located on the Chr10. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

H2afy2 H2A histone family, member Y2 [Mus musculus (house mouse)]

Gene ID: 404634, updated on 31-Jan-2019

Summary



Official Symbol H2afy2 provided by [MGI](#)

Official Full Name H2A histone family, member Y2 provided by [MGI](#)

Primary source [MGI:MGI:3037658](#)

See related [Ensembl:ENSMUSG00000020086](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as macroH2A2

Summary Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Nucleosomes consist of approximately 146 bp of DNA wrapped around a histone octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene encodes a replication-independent histone that is a member of the histone H2A family. It replaces conventional H2A histones in a subset of nucleosomes where it represses transcription and may participate in stable X chromosome inactivation. [provided by RefSeq, Nov 2015]

Expression Biased expression in CNS E11.5 (RPKM 57.9), whole brain E14.5 (RPKM 45.2) and 11 other tissues [See more](#)

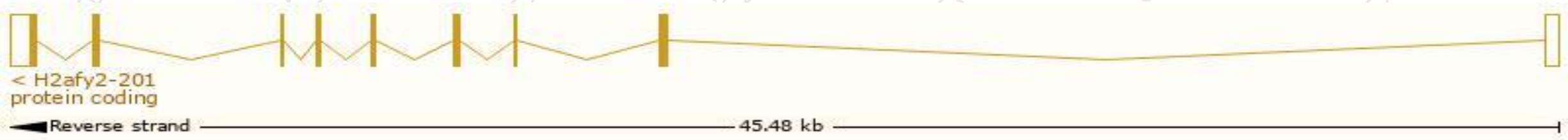
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

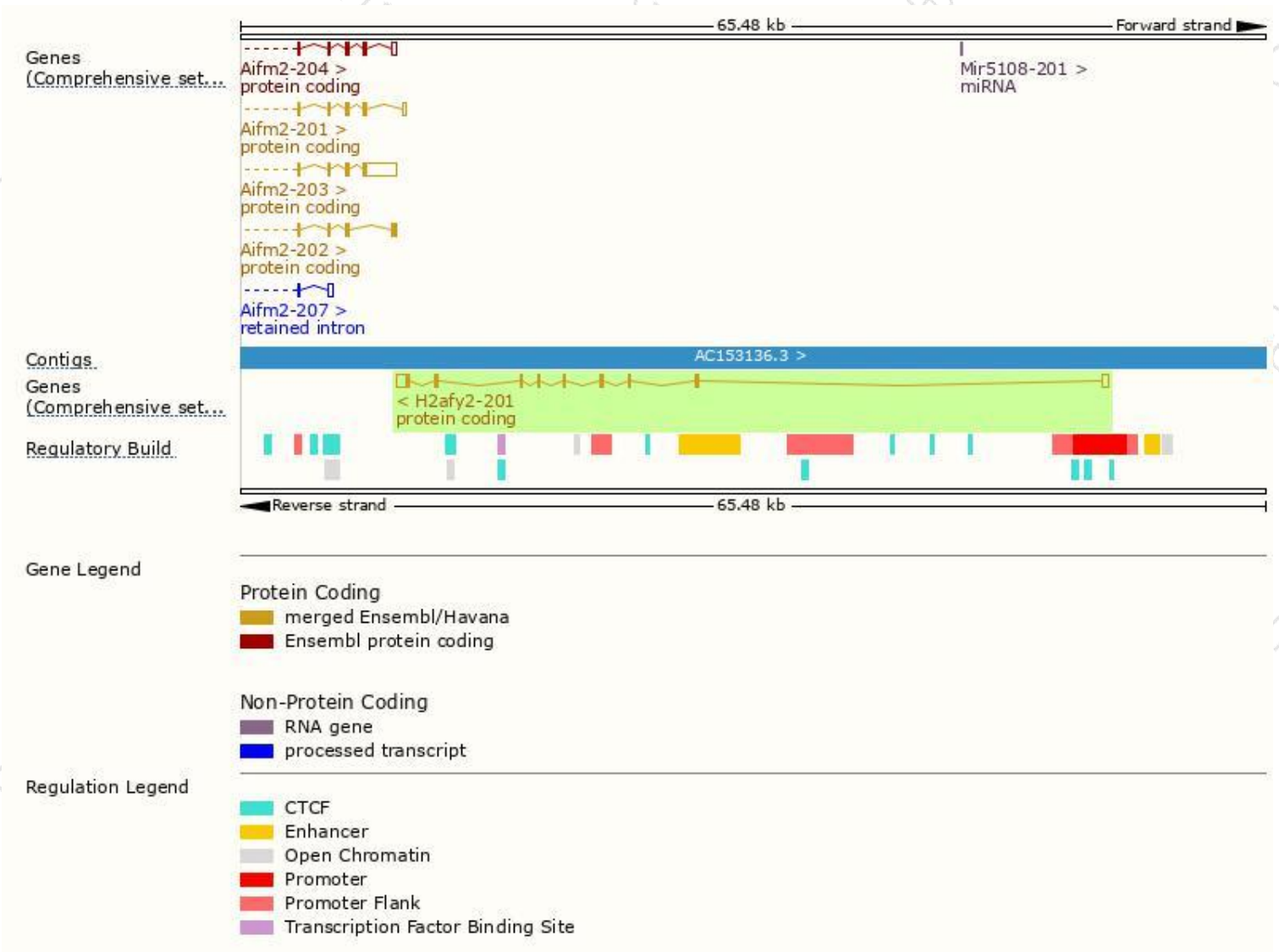
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
H2afy2-201	ENSMUST00000020283.4	2175	372aa	Protein coding	CCDS23885	Q8CCK0	TSL:1 GENCODE basic APPRIS P1

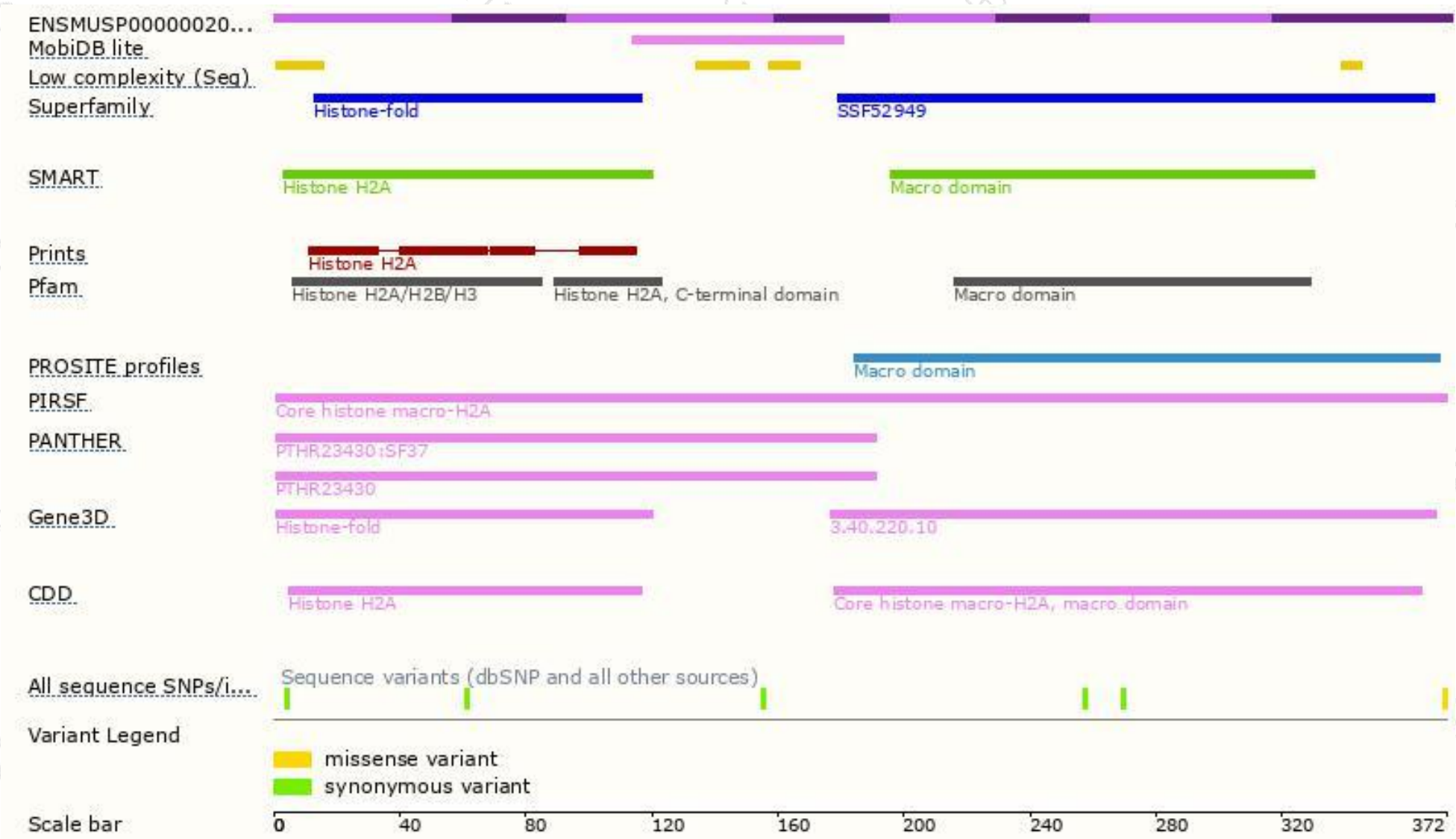
The strategy is based on the design of *H2afy2-201* transcript, The transcription is shown below



Genomic location distribution



Protein domain



If you have any questions, you are welcome to inquire.

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